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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/084,139

DATE: 12/26/2002
 TIME: 15:11:55

Input Set : A:\2002-12-06 1110-0307P.txt
 Output Set: N:\CRF4\12262002\J084139.raw

3 <110> APPLICANT: NAGATA, Shigekazu
 4 YATOMI, Takehiro
 5 SUDA, Takashi
 7 <120> TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT
 9 <130> FILE REFERENCE: 1110-0307P
 11 <140> CURRENT APPLICATION NUMBER: 10/084,139
C--> 12 <141> CURRENT FILING DATE: 2002-12-09
 14 <160> NUMBER OF SEQ ID NOS: 12
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
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 21 <213> ORGANISM: Mus sp.
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 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(381)
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 30 1 5 10 15
 32 ggt acc aga tgt gat atc cag atg aca cag act aca tcc tcc ctg tct 96
 33 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
 34 20 25 30
 36 gcc tct ctg gga gac aga gtc acc atc agt tgc agg gcc agt cag gac 144
 37 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
 38 35 40 45
 40 att agc aat tat tta aac tgg tat cag cag aaa cca gat gga act gtt 192
 41 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
 42 50 55 60
 44 aaa ctc ctg atc tac tac aca tca aga tta cac tca gga gtc cca tca 240
 45 Lys Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser
 46 65 70 75 80
 48 agg ttc agt ggc agt ggg tct ggg aca aat tat tct ctc acc att agc 288
 49 Arg Phe Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser
 50 85 90 95
 52 aac ctg gaa caa gga gat att gcc act tac ttt tgc caa cag ggt agt 336
 53 Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser
 54 100 105 110
 56 acg ctt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa 381
 57 Thr Leu Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 58 115 120 125
 61 <210> SEQ ID NO: 2
 62 <211> LENGTH: 127

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64 <213> ORGANISM: Mus sp.
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71     20          25          30
73 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
74     35          40          45
76 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
77     50          55          60
79 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
80     65          70          75          80
82 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser
83     85          90          95
85 Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser
86     100         105         110
88 Thr Leu Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
89     115         120         125
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93 <211> LENGTH: 408
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95 <213> ORGANISM: Mus sp.
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99 <222> LOCATION: (1)..(408)
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104     1           5           10          15
106 gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag    96
107 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
108     20          25          30
110 cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc   144
111 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
112     35          40          45
114 aca gaa tat cca atg cac tgg gtg aag cag gct cca gga aag ggt ttc   192
115 Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
116     50          55          60
118 aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct   240
119 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
120     65          70          75          80
122 gaa gag ttc aag ggg cgg ttt gcc ttc tct ttg gag acc tct gcc agc   288
123 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
124     85          90          95
126 act gcc tat ttg cag atc aac ttc ctc aaa aat gag gac acg gct aca   336
127 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
128     100         105         110
130 tat ttc tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggc caa   384

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Input Set : A:\2002-12-06 1110-0307P.txt

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131 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 132 115 120 125 408
 134 ggc acc act ctc aca gtc tcc tca
 135 Gly Thr Thr Leu Thr Val Ser Ser
 136 130 135
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 146 1 5 10 15
 148 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 149 20 25 30
 151 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 152 35 40 45
 154 Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
 155 50 55 60
 157 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 158 65 70 75 80
 160 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 161 85 90 95
 163 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 164 100 105 110
 166 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
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 169 Gly Thr Thr Leu Thr Val Ser Ser
 170 130 135
 173 <210> SEQ ID NO: 5
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 184 Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Leu Trp Val Pro 15
 185 1 5 10 15 96
 187 gga tca acc gga gat att cag atg acc cag agt ccg tcg acc ctc tct
 188 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 189 20 25 30
 191 gct agc gtc ggg gat agg gtc acc ata act tgc agg gca agt cag gac 144
 192 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
 193 35 40 45
 195 att tcg aat tat tta aac tgg tat cag cag aag cca ggc aaa gct ccc 192
 196 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 197 50 55 60
 199 aag ctt cta att tat tac aca tca aga tta cac tca ggg gta cct tca 240

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Input Set : A:\2002-12-06 1110-0307P.txt
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200 Lys Leu Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser
 201 65 70 75 80 288
 203 cgc ttc agt ggc agt gga tct ggg acc aat tat acc ctc aca atc tcg
 204 Arg Phe Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
 205 85 90 95
 207 agt ctg cag cca gat gat ttc gcc act tat ttt tgc caa cag ggt agt 336
 208 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
 209 100 105 110
 211 acg ctt ccg tgg acg ttc ggt cag ggg acc aag gtg gag gtc aaa 381
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 213 115 120 125
 216 <210> SEQ ID NO: 6
 217 <211> LENGTH: 127
 218 <212> TYPE: PRT
 219 <213> ORGANISM: Homo sapiens
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 222 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Trp Val Pro
 223 1 5 10 15
 225 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 226 20 25 30
 228 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
 229 35 40 45
 231 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 232 50 55 60
 234 Lys Leu Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser
 235 65 70 75 80
 237 Arg Phe Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
 238 85 90 95
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 248 <211> LENGTH: 408
 249 <212> TYPE: DNA
 250 <213> ORGANISM: Homo sapiens
 252 <220> FEATURE:
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 254 <222> LOCATION: (1)..(408)
 256 <400> SEQUENCE: 7
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 258 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
 259 1 5 10 15
 261 gcc caa gca cag gtc cag ttg gtg cag tct gga gct gag gtg aag aag 96
 262 Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 263 20 25 30
 265 cct gga agc tca gtc aag gtg tcc tgc aaa gct tct ggg tat acc ttc 144
 266 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 267 35 40 45

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Input Set : A:\2002-12-06 1110-0307P.txt
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269 aca gaa tat cca atg cac tgg gtg aga cag gct cca gga cag ggt ttc	192
270 Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe	
271 50 55 60	
273 aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct	240
274 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala	
275 65 70 75 80	
277 gaa gag ttc aag gga cgg ttt aca ttc act ttg gac acc tct acc aac	288
278 Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn	
279 85 90 95	
281 act gcc tat atg gag ctc agc tct ctc agg tct gag gac acg gct gtc	336
282 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
283 100 105 110	
285 tat tac tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggt caa	384
286 Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln	
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290 Gly Thr Leu Val Thr Val Ser Ser	
291 130 135	
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295 <211> LENGTH: 136	
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297 <213> ORGANISM: Homo sapiens	
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304 20 25 30	
306 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
307 35 40 45	
309 Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe	
310 50 55 60	
312 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala	
313 65 70 75 80	
315 Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn	
316 85 90 95	
318 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
319 100 105 110	
321 Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln	
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324 Gly Thr Leu Val Thr Val Ser Ser	
325 130 135	
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333 <220> FEATURE:	
334 <221> NAME/KEY: CDS	
335 <222> LOCATION: (36)..(1169)	
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/084,139

DATE: 12/26/2002

TIME: 15:11:56

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